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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      290
290
290
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282
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271
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198
198
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186
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match Length DB ID
   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-569-749-9
295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PEQLASAGFYYYGRNDDYKC.....CWESGDDPWVEHAKWFPRCE 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_plant:*
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sp_mammal:*
sp_mhc:*
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   195
197
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1140
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502
602
224
224
228
2379
2379
2376
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2376
2376
   13 091A70
13 091A69
13 091A69
13 091A69
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O94a70 gallus gall
O94a69 gallus gall
O57319 gallus gall
O57319 gallus gall
O94thl homo sapien
O94cc6 rattus norv
O95cs6 rattus norv
O95cs6 rattus norv
O95cs7 ansacta moo
O95hp7 homo sapien
O95ha8 homo sapien
O95ha8 homo sapien
O974b Ethoplus!
O94037 rattoplus!
O9677 spodoptera
O9674 buzura supp
O95877 spodoptera
O96715 mis miscall
O96860 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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44 75 25.4	43 75.5 25.6	42 76 25.8	41 77 26.3	40 77 26.1									. 110	115		119	121.5	130.5	131	131	160	171	174	174
4 87 4 87																								
11	u	12	υī					σ	12	12	12	12	12	12	1	12	υn	v	12	12	U	12	H	11
009123	Q9XZM7	Q9DVT5	Q18727	009119	Q22837	09DSW8	Q9DDK0	Q9GLN5	Q9PYQ9	61WA60	Q9PZ54	09YKL5	055770	092394	088738	Q9YVJ4	Q9VH01	Q9VEM2	Q91F18	Q9E232	Q9VUX5	Q9QES9	Q9EQ04	Q9EQ05
009123 mus musculu 009120 mus musculu	09xzm7 strongyloce	Q9dvt5 plutella xy	Q18727 caenorhabdi	009119 mus musculu	Q22837 caenorhabdi	Q9dsw8 ascovirus d	Q9ddk0 gallus gall	Q9gln5 sus scrofa	Ţ				055770 chilo iride	092394 bombyx mori	088738 mus musculu	Q9yvj4 melanoplus	Q9vh01 drosophila	Q9vem2 drosophila	Q91f18 helicoverps	Q9e232 helicoverpa	Q9vux5 drosophila	Q9qes9 epiphyas po	Q9eq04 rattus norv	Q9eq05 rattus norv

ALIGNMENTS

Qy Db	Ma Qu	S	DR.	닭닭	DR	DR	P. P.	PT.	3	e c	R P	RN	×	8	8	8	S	DE	DI	7	D.T	AC	ĬD	09IA70	DECL
1 PEOLASAGFYYVGRNDDVKCFCCDGGLRGWESGDDPWVEHAKWFPRCE 48	98.3%; Score 290; DB 13; Similarity 95.8%; Pred. No. 6.2e-30; 6; Conservative 1; Mismatches 1;	NON_TER 195 195 SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;	; PS		Pfam; PF00653; BIR; 2.		Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL: $AF221082$: $AAF35319.1$: .		"Genetic variation among chicken lines and mammalian species in	STRAIN-BREED DEGROUN, TIDDODESCHEDN;		[1]	NCBI_TaxID-9031;	Gallus.	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			(TremBLrel. 17,		2000	Q91A70;	Q91A70 PRELIMINARY; PRT; 195 AA.		Type 7

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SEQUENCE FROM N.A.

OF STAIN-WHITE LEACHORN; TISSUE-EMBRYONIC FIBROBLAST;

XX MEDILER-98038801; PubMed-9372964;

XX MEDILER-98038801; PubMed-9372964;

XX MODILER-98038801; PubMed-9372964;

XX MODILER-98038801; PubMed-9372964;

XX MODILER-98038801; PubMed-9372964;

XX MODILER-98038801; PubMed-9372964;

XY "CC1-INCTION: FIRE AND STAIN LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASH OF THE V-REL-TRANSFORMED CELLS.

CO -1- SUBCELLULAR LOCATION: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE STEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS SPLIENS THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN STEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN THE STEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN THE STEEN, THYMUS, BURSAIN, AND SKELETAL MUSCLE.

CO INTESTIS, BRAIN, AND SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P SEPOIENCE PROM N.A.

C STRAIN-BREED PAYOUNI: TISSUE-SPLEEN;

C STRAIN-BREED PAYOUNI: TISSUE-SPLEEN;

A ZhOU H., Lamont S.J.:

A ZhOU H., Lamont S.J.:

A SPECIFIC VARIABLION among Chicken lines and mammalian specife

PSPCHIFIC Genes.;

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ARZ21083; ARZ55320.1;

R INLECPTO; IPRO1370; BIR.

R INLECPTO; IPRO1370; BIR.

R PROSITE; PS01283; BIR, 2:

R PROSITE; PS01283; BIR, REPERT_1; 2.

R PROSITE; PS01283; BIR, REPERT_2; 2.

R PROSITE; PS1283; BIR, REPERT_2; 2.

R PROSITE; PS1283; BIR, REPERT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1NHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091A69;
091A69;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Archomauria: Aves; Neognathae: Galliformes; Phasianidae: Phasianinae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
NON_TER
NON_TER
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NCBI_TaxID-9031;
[1]
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01-0CT-2000 (TERMEIFEL 15, Last sequence update)
01-JUN-2001 (TERMEIFEL 17, Last annotation update)
INHIBITOR OF ADOPTOSIS 1 (FRAGMENT).
Gallus gallus (Chicken), Chordata; Cranlata; Vertebrata; Euteleostomi;
prologautia; Aves; Neosynathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PEQLASAGFYYYGRNDDVKCFCCDGGLRCWESGDDDWVEHAKWFPRCE 48
         PROCESS, THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC SIMILARITY: MEMBER OF THE IAP FAMILY.
SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEQLADAGEYYVGRNDDVKCFCCDGGLRCWESGDDPWIEHAKWEPRCE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 98.3%;
1 Similarity 95.8%;
46; Conservative
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197 /
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22602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 290; DB 13;
Pred. No. 6.3e-30;
1; Mismarches 1;
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                                                                                       EFFECT
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         RESULT OF REAL PROPERTY OF REAL PROPERTY
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Best Local S
Matches 46
InterPro; IPRO03376; Chapase.
InterPro; IPRO03376; Chapase.
InterPro; IPRO03598; ICE_p20.
InterPro; IPRO03598; Ig_c2.
InterPro; IPRO03509; Ig_like.
InterPro; IPRO03509; Ig_like.
InterPro; IPRO03509; Ig_like.
InterPro; IPRO03509; Ig_like.
InterPro; IPRO03508; Ig_like.
InterPro; IPRO03509; Ig_like; I,
SMART; SMO0115; CASC; I,
SMART; SMO0410; IG[c2; I,
SMART; SMO0410; IG[c2; I,
SMART; SMO0410; IG[c2; I].
SMART; SMO0410; IG[c3; I].
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1 SIMILARITY: CONTAINS A C3HC4
EMBL; AF008592; AAB88044.1; -.
HSSP; Q13490; 109H,
InterPro: ITRO01370; BIR.
InterPro: ITRO01370; BIR.
InterPro: ITRO01315; CARD:
InterPro: ITRO01301; BIR; 3
PEAM: PF00053; BIR; 3
PEAM: PF00059; CARD: 1.
SMART: SM00144; CARD: 1.
SMART: SM00144; ARD: 1.
SMART: SM00144; ARD: 1.
SMART: SM00144; ARD: 1.
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REEAT 30 97
REPEAT 176 242
REPEAT 262
REPEAT 262
ZN_EING 563 597
SEQUENCE 610 AA; 68924 MW; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MIDLINE-992772400; PubMed-10339464;

MIDLINE-992772400; PubMed-10339464;

Dierlamm J. Baens M. Wiodarska I., Stefanova-Ouzounova M. Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hagemelj Van den Berjabe H., Marynen P.;

"The apoptosis inhibitor gene APIZ and a novel 18q gene, ML "Ecutrently rearranged in the c(11:18)(q21:q21)p6ssociated uncosa-associated lymphoid tissue lymphomas."

Blood 93:3601-3609(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS01282: BIR_REPEAT_1;
PROSITE: PS50143: BIR_REPEAT_2;
PROSITE: PS50209: CARD: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF123094; AAD46161.1;
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I Similarity 95.8%;
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN REPEAT).
Y: CONTAINS A C3HC4-CLASS
2; AAB88044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIR REPEAT 1.
BIR REPEAT 2.
BIR REPEAT 3.
BIR REPEAT 3.
C3HC4-TYPE.
C3HC4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 290; DB 1
Pred. No. 2e-29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1140
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nunova M., Hagemeijer

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Matches

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Best Local S
Matches 45
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO01370; BIR.
InterPro; IPRO01370; CARD.
InterPro; IPRO01841; Znf_ring.
Pfam; PF00055; BIR; 3.
Pfam; PF00059; zf-C3HC4; 1.
Pfam; PF00099; zf-C3HC4; 1.
SMART; SM00144; CARD; 1.
SMART; SM00144; RING; 1.
SMART; SM00144; RING; 1.
PROSITE; PS0143; BIR_REPEAT_1; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                  OPESES PRELIMINARY, PRT; 589 AA.
OPESES;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLRel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0902C6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
INHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
MCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9QZC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; Q13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PEQLASAGFYYYGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEQLASAGFYYVGNSDDVKCFCCDGGLRCWESGDDPWVQHAKWFPRCE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEQLASAGEYYVDHNDDVKCFCCDGGLRCWEPGDDPWIEHAKWEPRCE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50143;
PS50208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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CASPASE_P20; 1.
.a; 128738 mW; 0C18D890287C723E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.6%;
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Pred. No. 4.2e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E6812FFE3EA34142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ww
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 589;
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                                                                    Rattus
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RESULT
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Best Local Similarity
Matches 44; Conserv
                                           Matches
                                                                  Query Match
Best Local
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Pfam; PF000619; CARD; 1.
Pfam; PF000619; Zf-C3HC4; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00214; CARD; 1.
SMART; SM00144; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 1.
PROSITE; PS50129; BIR_REPEAT_2; 3.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                            Pfam; PF00653; BIR; 3.

pfam; PF00097; zf-C3HC4; 1.

pfam; PF00097; zf-C3HC4; 1.

sMART; SM00218; BIR; 3.

sMART; SM00114; CARD; 1.

SMART; SM00114; CARD; 1.

PR0SITE; PS01282; BIR RBPEAT 1; 1

PR0SITE; PS01282; BIR RBPEAT 2; 3

PR0SITE; PS0209; CARD; 1.

Z100cfinger: 250209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPESE9 PRELIMINARY; PRT; 602 AA.
OPESE9;
01-MAR-2001 (TrembLrel. 16, Created)
01-MAR-2001 (TrembLrel. 17, Last sequence update)
01-JUN-2001 (TrembLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and Characterization of the Rat Homologs of the Inhibitor Apoptosis Protein 1, 2, and 3 Genes.";
Submitted (Sep-199) to the BMBL/Genebank/DDBJ databases.
-- SIMTLARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL, AF18431; AAG28971;
InterPro; IPR001375; CARD.
InterPro; IPR001375; CARD.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FF
Holcik M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
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1 PEQLASAGFYYYGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEQLASAGFYYYDHNDDVKCFCCDGGLRCWEPGDDPWIEHAKWFPRCE 306
                                              1 Similarity
43; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lefebvre C.A., Hicks K., Korneluk
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                                              Conservative
                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66750 MW;
                                                                                                                                                                 67326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.98;
                                                                  93.2%;
                                                                                                                                                                 M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 277; DB
; Pred. No. 9.4e
1; Mismatches
                                              w
••
                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B4F7089BD7CD285B
                                                                                                                                                                 CC91385EEA62DE5A CRC64;
                                           Mismatches
                                                                                                                                                                                                                                   ω μ
                                                                  e 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
.4e-28;
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01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 09, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
1.HILBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                          SEQUIENCE FROM N.A.
STRAIN-WISTAR: TISSUE-OVARY, CORPUS LUTEUN;
Bradley C.K., Lareu R.R., Dharmarajan A.M.;
Cloning and characterisation of an inhibitor of apoptosis protein
(IAP) in the rat corpus luteun.*;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF081503; AAG32497.1; -.
HSSP: Q13490, 10BH, 34497.1; -.
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                                                                                                                          InterPro; IPRO01370; BIR.
pro053; BIR; 2;
SMART; SM0023B; BIR; 2;
PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota: Metazoa: Chordata;
Mammalia: Eutheria: Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
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224 AA;
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; Galliformes; Phasianidae; Phasianinae;
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Sciurognathi; Muridae;
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Pl is a direct transcriptional target
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     213A52534D5EB56A CRC64;
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; Murinae; Rat
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InterPro; IPR0018170; BIR.
InterPro; IPR001811; Zof_ring.
Pfam; PP00553; BIR; 2.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
SEQUENCE 254 AA; 30547 MH; 2.
                                                                                                                                                                                                                                      O9HAP7
O9HAP7;
O9HAP7;
O1-MAR-2001 (TTEMBLICEL 16, C
O1-MAR-2001 (TTEMBLICEL 17, O1-TUN-2001 (TTEMBLICEL 17, O1-TUN-2001 (TTEMBLICEL 17, O1-TUN-2001 (TTEMBLICEL 17, O1-TUN-2001)
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Q9EN27;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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MEDLINE=20396580; PubMed=10936094;
MEDLINE=20396580; PubMed=10936094;
                                                                                                                                                                                                                   01-MAR-2001 (TIEMBLIEL 16) Last sequence update)
01-JUN-2001 (TIEMBLIEL 17) Last annotation update)
LIVIN INHIBITOR-OF-APOTOSIS (INHIBITOR OF APOPTOSIS)
(BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 7 (LIVIN))
                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete Genomic Sequence of the Amsacta moorel Entomopoxvirus Analysis and Comparison with Other Poxviruses."; Virology 274:120-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMV021
                     "Livin, a novel
                                        SEQUENCE FROM N.A. Kasof G.M., Gomes
                                                                                                        NCBI_TaxID-9606
                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                              LIVIN OR BIRC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bawden A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=28321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amsacta moorei
Viruses; dsDNA
Entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMV021
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1 (TrEMBLrel.
1 (TrEMBLrel.
                Gomes B.C.;
ovel inhibitor of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entomopoxvirus (AmEPV)
viruses, no RNA stage;
B.
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61.78;
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Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 198; DB 1
Pred. No. 7e-18;
0; Mismatches
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                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2EB72DA4B58D920A CRC64;
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No. 2.2e-19;
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                        family member. ";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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Submitted
[3]
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09H2A8; OTTEMBLIEL. 16, Created)
01-MAR-2001 (TremBLIEL. 16, Last sequence update)
01-UN-2001 (TremBLIEL. 17, Last annotation update)
101-JUN-2001 (TremBLIEL. 17, Last annotation update)
1NHIBITOR OF ADOPPOSIS PROTEIN KIAP (BA26INI1.1.2) (BACULOVIRAL IAP
REPERT-CONTAINING PROTEIN 7 (LIVIN), ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE
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280
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InterPro: IPRO01371; Znf_ring.
pfam; PF00653; BIR: 1.
pfam; PF00097; zf'C3RC4; 1.
SMART; SM0238; BIR; 1.
SMART; SM0238; BIR; 1.
PROSITE: PS0143; BIR; REPEAT_2; 1.
PROSITE: PS00518; ZINC_PINGER_C3HC4; UNKNOWN_1.
                                                                       -i- SIMILARITY: CONTAINS A RING-TYPE EMBL; AF301009; AAG37878.1; -EMBL; AJ309298; CAC37338.1; -EMBL; AL31827; CAC356111.1; -EMBL; AL21827; CAC356111.1; -InterPro; IPRO01370, BIR. InterPro; IPRO01370, BIR. InterPro; IPRO01370, BIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashhab Y., Alian A., Polliack A., Panet A., Ben-Yehuda D.; "Two splicing variants of a new inhibitor of apoptosis gene with different biological properties and tissue distribution pattern."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin J.-H., Deng G., Huang O., Morser J.;

*A Novel member of the inhibitor of apoptosis Biochem. Biophys. Res. Commun. 0:0-0(2000).
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"Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               Submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105
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PF000553; BIR; 1.
PF00097; zf-C3HC4; 1.
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30; Conser
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S A RING-TYPE ZINC FINGER.
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pred. No. 1.8e-17;
7; Mismatches 11
                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBj databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                  ZINC FINGER
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Matches 31
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Best Local
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                                                                                                                Q9U492
Q9U492;
01-MAY-2000 (1
01-MAY-2000 (1
01-JUN-2001 (1
INHIBITOR OF )
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Q9YNL8;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2001
IAP1.
Trichoplusia ni (Cabbage looper).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ingecta:
Eukaryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Pterygota; Neoptera; Endopterygota; Trichoplusia.
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SMART; SM00104; RING; 1.
PROSITE; PS00143; BIR, REPEAT_2; 1.
PROSITE; PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
SPROSITE; PS01282; BIR REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfan; PF00653; BIR; 2.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U82510; AAD00537.1;
HSSP; Q13490; 1QBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases -:- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
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SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lauzon H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10448;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 66.1
31; Conservative
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F APOPTOSIS PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                              PRELIMINARY;
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32090 MW;
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62.5%;
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66.0%;
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                                                                                                                     PROTEIN.
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17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear polyhedrosis virus (CfMNPV).
no RNA stage; Baculoviridae;
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Last sequence update)
Last annotation update)
                                                                                                                                                             Last
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Pred. No. 4.5e
5; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B2D9BE8A359F105E CRC64;
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..9e-17;
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.5e-17;
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RESULT

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RY MEDILINE-10062908; PubMed-10593985;
RX MEDILINE-10062908; PubMed-10593985;
RX MEDILINE-10062908; PubMed-10593985;
RX Seshagiri S., Vucic D., Lee J., Dixit V.M.;
Seshagiri S., Vucic D., Lee J., Dixit V.M.;
RX J. Biol. Chem. 274:36769-36773(1999).

RX InterPro; IPMO01370; BIR.

RX InterPro; IPMO01370; BIR.

RX InterPro; IPMO01370; BIR.

RX Prom. PRO0653; BIR; 2.

RX SMART; SMO0184; RING; 1.

RX PROSITE; PS00143; BIR.REPEAT_1; UNKNOWN_2.

SO SEQUENCE 379 AA; 41857 MM; 069381A012D9DE65 CRC64;
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                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.1%;
Best Local Similarity 61.7%;
Matches 29; Conservative
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MEDILINE-20144055; PubMed-10677478;
Huang O., Deveraux O.L., Macda S., Salvesen G.S., Stennicke H.R.,
Hammock B.D., Reed J.C.;

Evolutionary conservation of apoptosis mechanisms; Lepidopteran
baculoviral inhibitor of apoptosis proteins are inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spodoptera frugiperda (Fall armyworm). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Lepidoptera; Glossala; Ditrysia; Noctuoldea; Noctudae; Amphipyrinae; Spodoptera. NCBI_TaxID-7108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9N107: PRELIMINARY: PRT; 377 AA.
Q9N107: Q9N107: C1-C207-2000 (TrEMBLrel. 15, Created)
Q1-C27-2000 (TrEMBLrel. 15, Last sequence update)
Q1-UN-2001 (TrEMBLEEL. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN.
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[1]
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Conservative
                                                                                                                                                                                                      63.78;
                                                                                                                                                            Score 188; DB 5; Length 377; Pred. No. 2e-16; 7; Mismatches 11; Indels
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Pred. No. 1.5e-16;
7; Mismatches .11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 379;
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Search completed: January 7, 2002, 16:03:54 Job time: 1413 sec

